#2 OIPE

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/864,921 TIME: 14:54:31

Input Set : A:\Lj4752.txt
Output Set: N:\CRF3\06122001\I864921.raw

ENTERED

```
      4 <110> APPLICANT: Reed, John C.
      5       Pio, Frederick F.
      6       Godzik, Adam
      7       Stehlik, Christian
      8       Damiano, Jason S.
      9       Lee, Sug-Hyung
     10       Oliveira, Vasco A.
     11       Hayashi, Hideki
     12       Pawlowski, Krzysztof
     14 <120> TITLE OF INVENTION: Novel Card Domain Containing
     15       Polypeptides, Encoding Nucleic Acids, and Methods of Use
     18 <130> FILE REFERENCE: P-LJ 4752
C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/864,921
C--> 20 <141> CURRENT FILING DATE: 2001-05-23
     20 <150> PRIOR APPLICATION NUMBER: US 09/579,240
     21 <151> PRIOR FILING DATE: 2000-05-24
     23 <150> PRIOR APPLICATION NUMBER: US 09/686,347
     24 <151> PRIOR FILING DATE: 2000-10-10
     26 <150> PRIOR APPLICATION NUMBER: US 60/275,980
     27 <151> PRIOR FILING DATE: 2001-03-14
     29 <160> NUMBER OF SEQ ID NOS: 195
     31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     33 <210> SEQ ID NO: 1
     35 <400> SEQUENCE: 1
W--> 36  000
     38 <210> SEQ ID NO: 2
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W--> 41  000
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     45 <400> SEQUENCE: 3
W--> 46  000
     48 <210> SEQ ID NO: 4
     50 <400> SEQUENCE: 4
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     53 <210> SEQ ID NO: 5
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     63 <210> SEQ ID NO: 7
     65 <400> SEQUENCE: 7
W--> 66  000
     68 <210> SEQ ID NO: 8
     70 <400> SEQUENCE: 8
W--> 71  000
     73 <210> SEQ ID NO: 9
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RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/864,921 TIME: 14:54:31

Input Set : A:\Lj4752.txt
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     75 <400> SEQUENCE: 9
W--> 76  000
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W--> 81  000
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     84 <211> LENGTH: 1038
     85 <212> TYPE: DNA
     86 <213> ORGANISM: Homo sapien
     88 <220> FEATURE:
     89 <221> NAME/KEY: CDS
     90 <222> LOCATION: (1)...(930)
     92 <400> SEQUENCE: 11
     93 atg gct acc gag agt act ccc tca gag atc ata gaa aga gaa aga aaa   48
     94 Met Ala Thr Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys
     95  1               5                  10                  15
     97 aag ttg ctt gaa atc ctt caa cat gat cct gat tct atc tta gac acg   96
     98 Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr
     99              20                  25                  30
    101 tta act tct cgg agg ctg att tct gag gaa gag tat gag act ctg gag  144
    102 Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu
    103          35                  40                  45
    105 aat gtt aca gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta  192
    106 Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val
    107      50                  55                  60
    109 cag aaa aag gga gag gcg acc tgt cag cat ttt ctc aag tgt tta ttt  240
    110 Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe
    111  65                  70                  75                  80
    113 agt act ttt cca cag tca gct gcc att tgc ggc tta agg cat gaa gtt  288
    114 Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val
    115                  85                  90                  95
    117 tta aaa cat gag aat aca gta cct cct caa tct atg ggg gca agc agt  336
    118 Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser
    119             100                 105                 110
    121 aat tca gaa gat gct ttt tct cct gga ata aaa cag cct gaa gcc cct  384
    122 Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro
    123         115                 120                 125
    125 gag atc aca gtg ttc ttc agt gag aag gaa cac ttg gat ttg gaa acc  432
    126 Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr
    127     130                 135                 140
    129 tct gag ttt ttc agg gac aag aaa act agt tat agg gaa aca gct ttg  480
    130 Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu
    131 145                 150                 155                 160
    133 tct gcc agg aag aat gag aag gaa tat gac aca cca gaa gtc aca tta  528
    134 Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu
    135                 165                 170                 175
    137 tca tat tca gtt gag aaa gtt gga tgt gaa gtt cca gca act att aca  576
    138 Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr
    139             180                 185                 190
```

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Input Set : A:\Lj4752.txt
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```
141 tat ata aaa gat gga cag aga tat gag gag cta gat gat tct tta tac   624
142 Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr
143         195                 200                 205
145 tta gga aaa gag gaa tat cta gga tct gtt gac acc cct gaa gat gca   672
146 Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala
147     210                 215                 220
149 gaa gcc act gtg gaa gag gag gtt tat gat gac cca gag cac gtt gga   720
150 Glu Ala Thr Val Glu Glu Glu Val Tyr Asp Asp Pro Glu His Val Gly
151 225                 230                 235                 240
153 tat gat ggt gaa gag gac ttc gag aat tca gaa acc aca gag ttc tct   768
154 Tyr Asp Gly Glu Glu Asp Phe Glu Asn Ser Glu Thr Thr Glu Phe Ser
155                 245                 250                 255
157 ggt gaa gaa cca agt tat gag gga tca gaa acc agc ctt tca ttg gag   816
158 Gly Glu Glu Pro Ser Tyr Glu Gly Ser Glu Thr Ser Leu Ser Leu Glu
159             260                 265                 270
161 gag gaa cag gag aaa agt ata gaa ggc tgg tct cga act cat ggg ctt   864
162 Glu Glu Gln Glu Lys Ser Ile Glu Gly Trp Ser Arg Thr His Gly Leu
163         275                 280                 285
165 aag cga tcc tcc cac gtt ggc ctc cca aag tgc tgg gat tac agg cgt   912
166 Lys Arg Ser Ser His Val Gly Leu Pro Lys Cys Trp Asp Tyr Arg Arg
167     290                 295                 300
169 gag cca ccc tgc ctg gcc tgaaaattct gcctcaaaca tctcaaacat          960
170 Glu Pro Pro Cys Leu Ala
171 305                 310
173 ccatttatat tttgtacaag aaagtaaata aaatttttct ttttaacatt aaaaaaaaaa 1020
174 aaaaaaaaaa aatctaga                                            1038
176 <210> SEQ ID NO: 12
177 <211> LENGTH: 310
178 <212> TYPE: PRT
179 <213> ORGANISM: Homo sapien
181 <400> SEQUENCE: 12
182 Met Ala Thr Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys
183  1               5                  10                  15
184 Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr
185             20                  25                  30
186 Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu
187         35                  40                  45
188 Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val
189     50                  55                  60
190 Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe
191 65                  70                  75                  80
192 Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val
193                 85                  90                  95
194 Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser
195             100                 105                 110
196 Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro
197         115                 120                 125
198 Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr
199     130                 135                 140
```

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/864,921 TIME: 14:54:31

Input Set : A:\Lj4752.txt
Output Set: N:\CRF3\06122001\I864921.raw

```
200 Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu
201 145                 150                 155                 160
202 Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu
203                 165                 170                 175
204 Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr
205             180                 185                 190
206 Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr
207         195                 200                 205
208 Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala
209     210                 215                 220
210 Glu Ala Thr Val Glu Glu Glu Val Tyr Asp Asp Pro Glu His Val Gly
211 225                 230                 235                 240
212 Tyr Asp Gly Glu Glu Asp Phe Glu Asn Ser Glu Thr Thr Glu Phe Ser
213                 245                 250                 255
214 Gly Glu Glu Pro Ser Tyr Glu Gly Ser Glu Thr Ser Leu Ser Leu Glu
215             260                 265                 270
216 Glu Glu Gln Glu Lys Ser Ile Glu Gly Trp Ser Arg Thr His Gly Leu
217         275                 280                 285
218 Lys Arg Ser Ser His Val Gly Leu Pro Lys Cys Trp Asp Tyr Arg Arg
219     290                 295                 300
220 Glu Pro Pro Cys Leu Ala
221 305                 310
224 <210> SEQ ID NO: 13
226 <400> SEQUENCE: 13
W--> 227  000
229 <210> SEQ ID NO: 14
231 <400> SEQUENCE: 14
W--> 232  000
234 <210> SEQ ID NO: 15
236 <400> SEQUENCE: 15
W--> 237  000
239 <210> SEQ ID NO: 16
241 <400> SEQUENCE: 16
W--> 242  000
244 <210> SEQ ID NO: 17
246 <400> SEQUENCE: 17
W--> 247  000
249 <210> SEQ ID NO: 18
251 <400> SEQUENCE: 18
W--> 252  000
254 <210> SEQ ID NO: 19
256 <400> SEQUENCE: 19
W--> 257  000
259 <210> SEQ ID NO: 20
261 <400> SEQUENCE: 20
W--> 262  000
264 <210> SEQ ID NO: 21
266 <400> SEQUENCE: 21
W--> 267  000
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RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/864,921 TIME: 14:54:31

Input Set : A:\Lj4752.txt
Output Set: N:\CRF3\06122001\I864921.raw

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     269 <210> SEQ ID NO: 22
     271 <400> SEQUENCE: 22
W--> 272  000
     274 <210> SEQ ID NO: 23
     276 <400> SEQUENCE: 23
W--> 277  000
     279 <210> SEQ ID NO: 24
     281 <400> SEQUENCE: 24
W--> 282  000
     284 <210> SEQ ID NO: 25
     286 <400> SEQUENCE: 25
W--> 287  000
     289 <210> SEQ ID NO: 26
     291 <400> SEQUENCE: 26
W--> 292  000
     294 <210> SEQ ID NO: 27
     296 <400> SEQUENCE: 27
W--> 297  000
     299 <210> SEQ ID NO: 28
     301 <400> SEQUENCE: 28
W--> 302  000
     304 <210> SEQ ID NO: 29
     306 <400> SEQUENCE: 29
W--> 307  000
     309 <210> SEQ ID NO: 30
     311 <400> SEQUENCE: 30
W--> 312  000
     314 <210> SEQ ID NO: 31
     316 <400> SEQUENCE: 31
W--> 317  000
     319 <210> SEQ ID NO: 32
     321 <400> SEQUENCE: 32
W--> 322  000
     324 <210> SEQ ID NO: 33
     326 <400> SEQUENCE: 33
W--> 327  000
     329 <210> SEQ ID NO: 34
     331 <400> SEQUENCE: 34
W--> 332  000
     334 <210> SEQ ID NO: 35
     336 <400> SEQUENCE: 35
W--> 337  000
     339 <210> SEQ ID NO: 36
     341 <400> SEQUENCE: 36
W--> 342  000
     344 <210> SEQ ID NO: 37
     346 <400> SEQUENCE: 37
W--> 347  000
     349 <210> SEQ ID NO: 38
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VERIFICATION SUMMARY DATE: 06/12/2001
PATENT APPLICATION: US/09/864,921 TIME: 14:54:32

Input Set : A:\Lj4752.txt
Output Set: N:\CRF3\06122001\I864921.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1) SEQUENCE:
L:41 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:
L:46 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (3) SEQUENCE:
L:51 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (4) SEQUENCE:
L:56 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:61 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:66 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:71 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:76 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:81 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:227 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:232 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:237 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:242 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:247 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:252 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:257 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:262 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:267 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (21) SEQUENCE:
L:272 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (22) SEQUENCE:
L:277 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (23) SEQUENCE:
L:282 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (24) SEQUENCE:
L:287 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE:
L:292 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (26) SEQUENCE:
L:297 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (27) SEQUENCE:
L:302 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:
L:307 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (29) SEQUENCE:
L:312 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:317 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (31) SEQUENCE:
L:322 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (32) SEQUENCE:
L:327 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (33) SEQUENCE:
L:332 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (34) SEQUENCE:
L:337 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (35) SEQUENCE:
L:342 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (36) SEQUENCE:
L:347 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (37) SEQUENCE:
L:352 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (38) SEQUENCE:
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L:362 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE:
L:367 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (41) SEQUENCE:
L:372 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (42) SEQUENCE:
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L:382 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:387 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:392 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:397 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
L:402 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:

VERIFICATION SUMMARY DATE: 06/12/2001
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Input Set : A:\Lj4752.txt
Output Set: N:\CRF3\06122001\I864921.raw

L:407 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:412 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:417 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (51) SEQUENCE:
L:422 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (52) SEQUENCE: